

Formal Drawings:

The Office Action of July 18, 2000 and the current Office Action requested submission of formal drawings. Formal drawings are thus attached herein with this reply.

Nucleic Acid Sequence Listing:

The original application filed December 27, 1999 included a computer readable form and a printed form for the nucleic acid sequences referenced to in the present application, as well as a statement that the two sequence listings were identical. At the request of the Examiner, however, another copy of each is submitted with this response. Applicants respectfully submit that the requirements of 37 CFR §§ 1.821 through 1.825 have now been met.

In the Claims

Please amend claims 11, 57, and 64 to read as below, and add new claims 68 - 71.

In addition, please cancel claim 25 without prejudice.

11. (amended four times) A method for muting expression of an endogenous gene in a cultured population of animal cells, the method comprising the steps of:

(a) identifying a muting nucleic acid composition having a sequence that is homologous to a sequence in the endogenous gene, the nucleic acid composition being double stranded, or having the capacity to become double-stranded upon delivery to the population of cells, wherein identifying comprises the steps of:

(i) designating the entire gene sequence as the potential muting nucleic acid composition;

(ii) identifying muting fragments of the nucleic acid composition homologous to portions of the endogenous gene;

(b) delivering the muting nucleic acid into the population of cells; and

(c) muting expression of the endogenous gene wherein muting comprises muting at the level of post-transcription in the population as a whole, and wherein such muting is independent of integration, expression, or transcription of the delivered nucleic acid.

57. (once amended) A method for muting expression of an endogenous gene in a cultured population of animal cells, the method comprising:

(a) identifying a muting nucleic acid composition having a sequence that is homologous to a sequence in the endogenous gene, wherein the gene is one of a collagen, tumor necrosis factor (TNF), *tat*, and an immunoglobulin gene, the nucleic acid being double stranded, or having the capacity to become double-stranded upon delivery to the population of cells, wherein identifying comprises the steps of:

(i) designating the entire gene sequence as a potential muting nucleic acid composition;

(ii) identifying muting fragments of the nucleic acid composition homologous to portions of the endogenous gene;

(b) delivering the muting nucleic acid into the population of cells; and

(c) muting expression of the endogenous gene wherein muting comprises muting at the level of post-transcription in the population as a whole, and wherein such muting is independent of integration, expression, or transcription of the delivered nucleic acid.

68. (new) A method for muting expression of an endogenous gene in a population of animal cells, the method comprising the steps of:

(a) identifying a muting nucleic acid composition having a sequence that is homologous to a sequence in the endogenous gene, the nucleic acid composition being

double stranded, or having the capacity to become double-stranded upon delivery to the population of cells;

(b) delivering the muting nucleic acid into the population of cells; and

(c) muting expression of the endogenous gene, wherein muting comprises muting at the level of post-transcription in the population as a whole, and wherein such muting is independent of integration, expression, or transcription of the delivered nucleic acid.

69. (new) A method for muting expression of an endogenous gene in a population of animal cells, the method comprising:

(a) identifying a muting nucleic acid composition having a sequence that is homologous to a sequence in the endogenous gene, wherein the gene is one of a collagen, tumor necrosis factor (TNF), *tat*, and an immunoglobulin gene, the nucleic acid being double stranded, or having the capacity to become double-stranded upon delivery to the population of cells;

(b) delivering the muting nucleic acid into the population of cells; and

(c) muting expression of the endogenous gene, wherein muting comprises muting at the level of post-transcription in the population as a whole, and wherein such muting is independent of integration, expression, or transcription of the delivered nucleic acid.

70. (new) A method according to claim 68, wherein identifying further comprises:

(i) designating the entire gene sequence as a potential muting nucleic acid composition;

(ii) identifying muting fragments of the nucleic acid composition homologous to portions of the endogenous gene.